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# Involvement of Enterotoxins G and I in Staphylococcal Toxic Shock Syndrome and Staphylococcal Scarlet Fever

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We investigated the involvement of the recently described staphylococcal enterotoxins G and I in toxic shock syndrome. We reexamined *Staphylococcus aureus* strains isolated from patients with menstrual and nonmenstrual toxic shock syndrome (nine cases) or staphylococcal scarlet fever (three cases). These strains were selected because they produced none of the toxins known to be involved in these syndromes (toxic shock syndrome toxin 1 and enterotoxins A, B, C, and D), enterotoxin E or H, or exfoliative toxin A or B, despite the fact that superantigenic toxins were detected in a CD69-specific flow cytometry assay measuring T-cell activation. Sets of primers specific to the enterotoxin G and I genes (*seg* and *sei*, respectively) were designed and used for PCR amplification. All of the strains were positive for *seg* and *sei*. Sequence analysis confirmed that the PCR products, corresponded to the target genes. We suggest that staphylococcal enterotoxins G and I may be capable of causing human staphylococcal toxic shock syndrome and staphylococcal scarlet fever.

Toxic shock syndrome (TSS) is a life-threatening multisystem disorder caused by strains of *Staphylococcus aureus*. It is characterized by rapid onset of fever, arterial hypotension, scarlatiniform rash, and multiorgan failure (4). Originally described for children by Todd and Fishaut in 1978 (32), TSS has been extensively studied over the past 18 years, since the occurrence of major outbreaks associated with menstruation and the use of a newly introduced superabsorbant brand of tampon (3, 4). These tampons were withdrawn from the market, and most cases of TSS now occur in settings other than menstruation and among individuals of both sexes and all ages. Nonmenstrual TSS is usually secondary to *S. aureus* infection or to skin or mucosal trauma with *S. aureus* colonization (4).

S. aureus TSS toxin 1 (TSST-1) was the first toxin shown to be involved in TSS, in both menstrual and nonmenstrual cases (2, 30). Staphylococcal enterotoxins A to D and H (SEA to SED and SEH) also appear to have caused some cases of nonmenstrual TSS (8, 14, 16, 21, 28, 29). TSST-1 and SEA to SED have been linked to other staphylococcal syndromes such as staphylococcal scarlet fever (SSF) and recalcitrant erythematous desquamating disorder (REDD), both of which were suggested to be variants of TSS on the basis of toxin production and certain clinical similarities (6, 18). Another staphylococcal enterotoxin (SEE) was isolated from chicken and food specimens but has not been associated with TSS (7). All of these toxins exhibit superantigen activity, stimulating polyclonal Tcell proliferation through coligation between major histocompatibility complex class II molecules on antigen-presenting cells and the variable portion of the T-cell antigen receptor B chain (22). This superantigen activity can be detected with mitogenic assays (with mouse, rabbit, or human leukocytes) or in a CD69-specific flow cytometric assay of T-cell activation (15, 17).

In a French epidemiological survey of *S. aureus* isolates from patients with TSS, SSF, and REDD, several strains produced

none of the known superantigenic toxins (TSST-1, SEA to SEE, and SEH), but superantigen activity was detected in culture supernatants in a CD69-specific flow cytometric assay, pointing to unknown superantigenic toxins (16). Recently, two new staphylococcal enterotoxins, SEG and SEI, have been isolated from *S. aureus* strains collected from human nares but have not been linked to TSS (24). In this study we used PCR to detect the SEG and SEI genes (*seg* and *sei*, respectively) in CD69-positive, SEA- to SEE-, SEH-, and TSST-1-negative strains isolated from patients with a diagnosis of TSS or SSF. *seg* and *sei* were detected in all of these strains, suggesting a clinical importance for these new toxins.

## MATERIALS AND METHODS

**Patients.** The 12 patients included in this study corresponded to nine cases of TSS (including two menstrual case) and three cases of SSF. They were all colonized or infected by *S. aureus* strains that did not produce the usual superantigenic toxins associated with TSS. They were selected from among 170 cases of TSS, 5 cases of REDD, and 105 cases of SSF reported to the Centre National de Référence des Toxémies à Staphylocoques (Lyon, France) between 1 January 1985 and 31 January 1999 from hospitals throughout France. Cases were first identified by chart review if the patient was from the Lyon area or otherwise from accompanying notes sent to the staphylococcal reference center. Cases met the definition of TSS, REDD, or SSF (4, 6, 16). The patients were epidemiologically unrelated.

**Strains.** *S. aureus* strains from patients with TSS or SSF were cultured from sites including the genital tract, blood, skin, throat, and soft tissues. Strains were identified as *S. aureus* by their ability to coagulate citrated rabbit plasma (bioMérieux, Marcy-l'Etoile, France) and to produce a clumping factor (Staphyslide test; bioMérieux). Isolates were typed by using phage and serotyping techniques (33).

Toxins. Superantigen activity in culture supernatants was detected by measuring T-cell activation in a CD3- and CD69-specific flow cytometry assay (15). Since fewer than 1% of unstimulated CD3<sup>+</sup> lymphocytes spontaneously expressed CD69, T cells were considered to be activated when more than 2% expressed CD69 (15).

Sequences specific for sea to see, seg to sei, eta, etb, and tst, encoding SEA to SEE, SEG to SEI, exfoliative toxin A (ETA), ETB, and TSST-1, respectively, were detected by PCR. Genomic DNA was extracted from staphylococcal cultures and used as a template for amplification with the primers described in Table 1 (Eurogentec, Seraing, Belgium). The thermal conditions were as follows: denaturation for 1 min at 94°C, annealing for 1 min at 55°C, and extension for 1 min at 72°C. Amplification of gyrA (11) was used as a control to confirm the quality of each DNA extract and the absence of PCR inhibitors. All PCR products were analyzed by electrophoresis through 1% agarose gels (Sigma, Saint Quentin Fallavier, France). The following S. aureus strains were used to

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TABLE 1. Base sequences of the staphylococcal toxin-specific oligonucleotide primers and predicted sizes of amplified products

Gene <sup>a</sup>	GenBank accession no.	Primer	Oligonucleotide sequence $(5' \rightarrow 3')$	Size of amplified product <sup>b</sup> (bp)	Reference
sea	M18970	SEA-1	TTGGAAACGGTTAAAACGAA	120	12
		SEA-2	GAACCTTCCCATCAAAAACA		
seb	M11118	SEB-1	TCGCATCAAACTGACAAACG	478	12
		SEB-2	GCAGGTACTCTATAAGTGCC		
sec	X05815	SEC-1	GCATAAAAGCTAGGAATTT	257	12
		SEC-2	AAATCGGATTAACATTATCC		
sed	M28521	SED-1	CTAGTTTGGTAATATCTCCT	317	12
		SED-2	TAATGCTATATCTTATAGGG		
see	M21319	SEE-1	CAAAGAAATGCTTTAAGCAATCTTAGGCCAC	482	12
		SEE-2	CTTACCGCCAAAGCTG		
seg	AF064773	SEG-1	AATTATGTGAATGCTCAACCCGATC	642	This study
		SEG-2	AAACTTATATGGAACAAAAGGTACTAGTTC		
seh	U11702	SEH-1	CAATCACATCATATGCGAAAGCAG	375	This study
		SEH-2	CATCTACCCAAACATTAGCACC		
sei	AF064774	SEI-1	CTCAAGGTGATATTGGTGTAGG	576	This study
		SEI-2	AAAAAACTTACAGGCAGTCCATCTC		
tst	J02615	TSST-1	ATGGCAGCATCAGCTTGATA	350	12
		TSST-2	TTTCCAATAACCACCCGTTT		
eta	M17347	ETA-1	CTAGTGCATTTGTTATTCAA	119	12
		ETA-2	TGCATTGACACCATAGTACT		
etb	M17348	ETB-1	ACGGCTATATACATTCAATT	200	12
		ETB-2	TCCATCGATAATATACCTAA		

<sup>&</sup>lt;sup>a</sup> Genes encoding SEA to SEE, SEG to SEI, TSST-1, ETA, and ETB.

control the specificity of PCR amplification: RN-450 (negative control), A970237 (negative control), A990204 (negative control), FDA-S6 (ATCC 13566) (sea +), FRI-137 (ATCC 19095) (sec+), FRI-1151m (sed+), FRI-326 (ATCC 27664) (see<sup>+</sup>), FRI-569 (ATCC 51811) (seh<sup>+</sup>), FRI-1169 (tst<sup>+</sup>), TC-7 (eta<sup>+</sup>), and TC-146 (etb<sup>+</sup>) (1, 7, 11, 13, 15, 20, 26, 27, 31). Since no control strains for SEG and SEI were available, the specificity of seg and sei amplification was assessed by DNA sequencing of selected PCR products (Genome Express, Grenoble, France). To rule out the possibility of false-negative PCRs due to minor variations in the DNA sequences, Southern blotting of selected strains was performed as follows: total DNA was digested with HindIII (Boehringer Mannheim, Meylan, France), separated on a 1% agarose gel, vacuum transferred to positively charged nylon membranes (Boehringer Mannheim), and cross-linked by exposure to UV light. The seg and sei PCR products were labelled with digoxigenin (DIG) by using a DIG DNA Labelling and Detection Kit (Boehringer Mannheim) for use as probes. Hybridization and washing steps were carried out at 68°C in standard buffer solutions (Boehringer Mannheim). Hybridizing bands were detected with anti-DIG-alkaline phosphatase conjugate and the chemiluminescent substrate CSPD, using the DIG Luminescent Detection kit in accordance with the instructions of the supplier (Boehringer Mannheim). Lumi-Film (Boehringer Mannheim) was subsequently exposed to the membranes for 1 h. The sizes of the hybridizing bands were estimated by using a 1-kb DNA ladder (Gibco BRL, Cergy Pontoise, France).

## **RESULTS**

The 12 *S. aureus* strains induced CD69 expression by over 2% of CD3<sup>+</sup> lymphocytes (Table 2), in a manner similar to that observed with supernatants from control strains producing known superantigenic toxins (Table 3). In contrast, the toxinnegative control strain (RN450) induced CD69 expression in only  $0.4\% \pm 0.2\%$  of CD3<sup>+</sup> lymphocytes, as observed with strains that do not produce superantigenic toxins (15).

The 12 strains were examined for the presence of sea to see, seg to sei, eta, and etb by PCR amplification, and were all positive for seg and sei only (Table 2), while RN-450 was negative for all of these genes. Several of the control strains harboring sea to see, seh, tst, eta, or etb were also positive for both seg and sei (Table 3). seg and sei amplicons from 3 of the 12 clinical strains were sequenced, and the sequences were 100% identical to the published sequences (GenBank accession no. AF064773 and AF064774, respectively). Since a change in only a few bases could cause false-negative results in

seg or sei PCRs, DNAs from three PCR-positive strains and five PCR-negative strains were analyzed by Southern blotting with seg and sei probes. Only strains which were positive for seg and sei by PCR hybridized to both DNA probes (Fig. 1), thus confirming the PCR results. The sizes of the hybridizing fragments were identical for both probes but differed between strains, from ≈2.9 kb (strains A900322 and TC7) to >7.1 kb (strain A980483) (Fig. 1).

Since all 12 strains were positive for both genes by PCR and the sizes of the hybridizing fragments were identical for both probes, the possibility that the *seg* and *sei* loci were adjacent to each other was investigated by attempting to coamplify the two genes with all combinations of *seg*- and *sei*-specific primers. Only the combination of primer SEI-1 with primer SEG-2 produced an amplicon, of about 3.2 kb, while the other primer combinations gave negative results. Partial sequence analysis showed that the 3.2-kb amplicon contained portions of both *seg* and *sei*, in tandem orientation with a 1.9-kb intergenic segment.

Eight of the clinical strains harboring *seg* and *sei* were analyzed by phage typing and serotyping. They were not clonal, as they had distinct phage types. Four strains belonged to phage group III, one belonged to group V, and three were untypeable (Table 2). Serotyping confirmed the absence of clonality.

## DISCUSSION

Among the staphylococcal superantigenic toxins, only TSST-1, SEA, SEB, SEC, and SED have been linked to TSS or SSF (8, 18, 21). This study shows that two additional staphylococcal enterotoxins, SEG and SEI, are likely associated with human TSS and SSF. We selected strains of *S. aureus* isolated from patients with TSS or SSF and which did not produce TSST-1, SEA to SEE, SEH, ETA, or ETB. Using PCR amplification with primer sets designed to be specific for *seg* or *sei*, we detected both genes in all 12 strains and also in several control strains (Tables 2 and 3). The specificity of *seg* and *sei* amplification was confirmed by sequence analysis of PCR

<sup>&</sup>lt;sup>b</sup> Size of PCR product derived from published GenBank sequences.

TABLE 2. Toxin production by S. aureus isolates from patients with TSS or SSF that do not produce TSST-1, SEA to SEE, SEH, ETA, or ETB

Case strain strain      S. aureus. Solitive sample(s) and D3+T con CD3+T con CD3+T con CD3+T strain      Tokage strain strain      CD69 expression con CD3+T				Bacterial	Bacterial characteristics				Patient characteristics	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	Case		S. aureus-positive sample(s)	CD69 expression on CD3 <sup>+</sup> T cells <sup>a</sup> (%)		Serotype		Age (yr)/sex	Clinical manifestation(s)	Outcome
, and 6.1 ± 0.3 SEG, SEI $c_1/o/1$ Group V: 94/96 17/M 6.1 ± 0.3 SEG, SEI $c_1/o/1$ Group III: 84 27/F 17/H 7.4 ± 2.9 SEG, SEI $c_1/o$ Group III: 29/52/52A/79/80/47/ 18/F 5.2 ± 2.0 SEG, SEI $c_1/o$ Group III: 29/52/52A/79/80/47/ 18/F 38/51 2.0 SEG, SEI $c_1/o$ Group III: 53/54/83A/85 23/M 39/F 31 ± 0.8 SEG, SEI $c_1/O$ Unitypeable 15/9 SEG, SEI $c_1/O$ Group III/D: 53/77/83A/84/85/87 9/F 8.6 ± 2.6 SEG, SEI $c_1/O$ ND ND 39/F 39/F 8.8 ± 0.5 SEG, SEI ND ND ND 2/F 35/M 2.7 ± 0.7 SEG, SEI ND ND ND 2/F 35/M 2.7 ± 0.7 SEG, SEI ND ND ND 2/F 35/M 2.7 ± 0.7 SEG, SEI ND ND ND 2/F 35/M 2.7 ± 0.7 SEG, SEI ND ND ND 2/F 35/M 34/F	1	A850375	Blood	$4.4 \pm 1.6$	SEG, SEI	$h_2/m/1$	Untypeable	77/M	Arteriovenous shunt abscess, TSS	Dead
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	7	A860376	Abscess	$3.2 \pm 0.6$	SEG, SEI	$c_1/0/1$	Group V: 94/96	17/M	Thigh abscess, TSS	Alive
	$\omega$	A890326		$6.1 \pm 0.3$	SEG, SEI	$c_1/i_1i_2/o$	Group III: 84	27/F	Puerperal SSF	Mother alive, newborn dead
Pharymx      5.2 ± 2.0      SEG, SEI      e/h <sub>2</sub> /o/262-3      Untypeable      19/F        Blood, bronchoalveolar lavage, cerebrospinal fluid      5.9 ± 0.9      SEG, SEI      c <sub>1</sub> /o      Group III: 53/54/83A/85      23/M        Urine Vine      2.9 ± 1.1      SEG, SEI      c <sub>1</sub> /l      Untypeable      15/M        Pus      2.9 ± 1.1      SEG, SEI      c <sub>1</sub> Group III/D: 53/77/83A/84/85/87      9/F        Wound      8.6 ± 2.6      SEG, SEI      ND      ND      39/F        Pharymx      2.7 ± 0.7      SEG, SEI      ND      ND      2/F        Tampon, vagina, blood      5.3 ± 1.2      SEG, SEI      ND      ND      2/F	4	A900322	Tampon, vagina	$7.4 \pm 2.9$	SEG, SEI	$c_1/o$	Group I/III: 29/52/52A/79/80/47/ 53/54/83A/84/85	18/F	Menstrual TSS	Alive
Blood, bronchoalveolar      5.9 ± 0.9      SEG, SEI      c <sub>1</sub> /o      Group III: 53/54/83A/85      23/M        lavage, cerebrospinal fluid      3.1 ± 0.8      SEG, SEI      c <sub>1</sub> /l      Untypeable      15/M        Urine      2.9 ± 1.1      SEG, SEI      c <sub>1</sub> /l      Group III/D: 53/77/83A/84/85/87      9/F        Sinus, blood      8.6 ± 2.6      SEG, SEI      ND      ND      39/F        Wound      8.8 ± 0.5      SEG, SEI      ND      ND      35/M        Pharynx      2.7 ± 0.7      SEG, SEI      ND      ND      2/F        Tampon, vagina, blood      5.3 ± 1.2      SEG, SEI      ND      ND      44/F	2	A900422		$5.2 \pm 2.0$			Untypeable	19/F	Pharyngitis, SSF	Alive
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	9	A910472	B	$5.9 \pm 0.9$		$c_1/o$	Group III: 53/54/83A/85	23/M	Bacteriemia, pneumonia, meningitis, and TSS in an intravenous-drug user	Alive
Pus      2.9 ± 1.1      SEG, SEI      c1      Group III/D: 53/77/83A/84/85/87      9/F        Sinus, blood      8.6 ± 2.6      SEG, SEI      ND      ND      39/F        Wound      8.8 ± 0.5      SEG, SEI      ND      35/M        Pharynx      2.7 ± 0.7      SEG, SEI      ND      2/F        Tampon, vagina, blood      5.3 ± 1.2      SEG, SEI      ND      ND      44/F	_	A930316		$3.1 \pm 0.8$	SEG, SEI	$c_1/l$	Untypeable	15/M	Postendoscopy urinary tract infection, TSS	Alive
Sinus, blood $8.6\pm2.6$ SEG, SEI ND $^c$ ND $39/F$ SVound $8.8\pm0.5$ SEG, SEI ND ND $35/M$ Sharynx $2.7\pm0.7$ SEG, SEI ND ND $2/F$ Tampon, vagina, blood $5.3\pm1.2$ SEG, SEI ND ND $2/F$ $44/F$	∞	A950260		$2.9 \pm 1.1$	SEG, SEI	$c_1$	Group III/D: 53/77/83A/84/85/87	9/F	Infection of finger pulp, TSS	Alive
Wound $8.8\pm0.5$ SEG, SEI ND ND $35/M$ Pharynx $2.7\pm0.7$ SEG, SEI ND ND $2/F$ Tampon, vagina, blood $5.3\pm1.2$ SEG, SEI ND ND $2/F$ $44/F$	6	A980044	Sinus, blood	$8.6 \pm 2.6$	SEG, SEI	$ND^c$	ND	39/F	Sinusitis, TSS	Alive
Pharynx 2.7 ± 0.7 SEG, SEI ND ND 2/F Tampon, vagina, blood 5.3 ± 1.2 SEG, SEI ND ND 44/F	10	A980114	Wound	$8.8 \pm 0.5$	SEG, SEI	ND	ND	35/M	Postoperative spondylitis, TSS	Alive
Tampon, vagina, blood $5.3 \pm 1.2$ SEG, SEI ND ND $44/F$	11	A980483		$2.7 \pm 0.7$	SEG, SEI	ND	ND	2/F	Pharyngitidis, SSF	Alive
	12	A990055		$5.3 \pm 1.2$	SEG, SEI	ND	ND	44/F	Menstrual TSS	Dead

"The percentage of CD69-positive cells was determined after electronic gating of the CD3<sup>+</sup> population. All experiments used separate blood samples from one donor. Results are shown as means ± standard deviations All toxins were detected by PCR assay of the corresponding genes

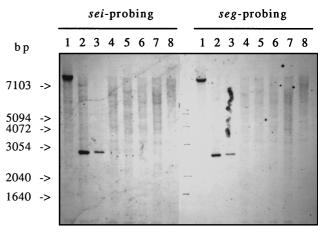


FIG. 1. Southern blot hybridization of DNAs of *S. aureus* strains with *sei* and *seg* probes. Total DNA was digested with *Hin*dIII, separated by agarose gel electrophoresis, transferred to positively charged nylon membranes, and probed with the indicated DIG-labelled probes. Lanes contain DNAs of three *S. aureus* strains found to be PCR positive for *seg* and *sei* (lanes 1, A980483; lanes 2, TC-7; and lanes 3, A900322) and five *S. aureus* strains found to be PCR negative for *seg* and *sei* (lanes 4, FRI-1169; lanes 5, FRI-569; lanes 6, RN-450; lanes 7, A970237; and lanes 8, A990204).

products and Southern blotting (Fig. 1). SEG and SEI produced by these strains were probably responsible for the T-cell activation detected in a CD69-specific flow cytometry assay. It is also conceivable that the SEG and SEI produced by these strains caused the clinical manifestations of TSS or SSF.

As seg and sei were initially cloned from two different strains (FRI-572 and FRI-445, respectively) (24), we were surprised that both seg and sei were detected in all 12 clinical strains and also in several reference strains (Table 3). The positive PCR amplification obtained with the SEI-1 and SEG-2 primers in our study indicates that sei and seg are in tandem orientation and are separated by 1.9 kb of intergenic DNA. Sequencing of this intergenic region is under way to determine whether it contains additional open reading frames, as suggested by the reported observation that strain FRI-445 contains part of an enterotoxin-like gene upstream of sei (24). The link between two staphylococcal superantigenic toxins such as seg and sei is not uncommon; it has been described for plasmid pIB485, which contains both sed and sej (34), and for pathogenicity islands containing both tst and an enterotoxin-like gene (19). Phage typing and serotyping ruled out a clonal origin of our S. aureus clinical strains harboring seg and sei and responsible for TSS, contrasting with the clonal origin of strains isolated from patients with menstrual TSS that produced TSST-1 (25).

Three of the strains that produced SEG and SEI were associated with two cases of menstrual TSS and a case of puerperal SSF, respectively. Previous findings suggested that the vast majority of cases of menstrual TSS were due to TSST-1-producing strains (29). However, some vaginal isolates from women with menstrual TSS did not produce TSST-1, suggesting that other staphylococcal toxins might be responsible for the clinical manifestations (4, 9, 10, 21); indeed, cases of menstrual TSS related to strains producing only SEA to SED have been described (8, 23). Our data suggest that *S. aureus* strains producing SEG and SEI but not TSST-1 can also cause menstrual TSS, although this needs to be confirmed by experimental and epidemiological studies.

In conclusion, *S. aureus* strains that produce both SEG and SEI may be associated with SSF and TSS (including menstrual cases), and the SEG and SEI determinants are close to each other on the *S. aureus* chromosome. The PCR amplification

Control strain	Reference	CD69 expression on CD3 <sup>+</sup> T cells (%) <sup>a</sup>	Toxin production detected in this study <sup>b</sup>											
(reference)	toxin production		SEA	SEB	SEC	SED	SEE	SEG	SEH	SEI	TST	ETA	ETB	
RN-450 (26)	None	$0.5 \pm 0.2$	_	_	_	_	_	_	_	_	_	_	_	
FDA-S6 (20)	SEA, SEB	$14.7 \pm 2.2$	+	+	_	_	_	_	_	_	_	_	_	
FRI-137 (27)	SEC	$4.9 \pm 1.5$	_		+	_	_	+	+	+	_	_	_	
FRI-1151m (13)	SED	$5.0 \pm 1.8$	_	_	_	+	_	_	_	_	_	_	_	
FRI-326 (7)	SEE	$9.8 \pm 1.7$	_	_	_	_	+	_	_	_	_	_	_	
FRI-569 (31)	SEH	$2.3 \pm 0.2$	_	_	_	_	_	_	+	_	_	_	_	
FRI-1169 (5)	TSST-1	$7.3 \pm 1.2$	_	_	_	_	_	_	_	_	+	_	_	
TC-7 (1)	ETA	$10.5 \pm 1.8$	_	_	_	_	_	+	_	+	_	+	_	
TC-146 (1)	ETB	$5.7 \pm 1.2$	_	_	_	_	_	+	_	+	_	_	+	

TABLE 3. Toxin production by S. aureus control strains

method used in this study is an efficient way of identifying strains harboring seg and sei.

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<sup>&</sup>lt;sup>a</sup> See footnote a of Table 2.

<sup>&</sup>lt;sup>b</sup> See footnote b of Table 2.